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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/002,278

DATE: 04/08/2002
TIME: 09:26:20

Input Set : A:\40314-a.txt
Output Set: N:\CRF3\04082002\J002278.raw

ENTERED

3 <110> APPLICANT: Jessell, Thomas M.
4 Basler, Konard
5 Yamada, Toshiya
7 <120> TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF DORSALIN-1
9 <130> FILE REFERENCE: 0575/40314-A
11 <140> CURRENT APPLICATION NUMBER: 10/002,278
12 <141> CURRENT FILING DATE: 2001-11-02
14 <160> NUMBER OF SEQ ID NOS: 18
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1603
20 <212> TYPE: DNA
21 <213> ORGANISM: Chick
23 <400> SEQUENCE: 1
24 cctttcctct gtctgtaaag attcaacatt tttaatcagt taaaatactt tgtcctcttg 60
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28 tctgttttca atatcattgc ctgcctgaca agaggcaagc ctttggaata ctggaaaaag 180
30 ctaccagtta tggaagagtc tgatgcattc tttcatgata ctggggaagt ggaacatgac 240
32 acccaacttg actttaaatc tttcttggag aatatgaaga cagatttact aagaagtctg 300
34 aatttatcaa ggggtccctc acaagtgaag accaaagaag agccaccaca gtatcatgatt 360
36 gatttatata acagatatat agcggacaag tcttccatcc ctgcatccaa catcgtgagg 420
38 agcttcagca ctgaagatgt tgtttcttta atttcaccag aagaacactc atttcagaaa 480
40 cacatcttgc tcttcaacat ctctattcca cgatatgagg aagtcaccag agctgaactg 540
42 agaattctta tctcctgtca caaggaagtt ggggtctccct ccagactgga aggcaacatg 600
44 gtcattttatg atgttctaga tggagacat tgggaaaaca aagaaagtac caaatcttta 660
46 ctgtgtctct acagtattca ggactgtggc tgggagatgt ttgaggtgtc cagcgtgtgt 720
48 aaaagatggg tcaaggcaga caagatgaag actaaaaaca agctagaggt tgttatagag 780
50 agtaaggatc tgagtgtttt tcttgttggg aagctggata ttactgttac tcatgacact 840
52 aaaaatctgc ccctattaat agtgttctcc aatgatcgca gcaatgggac aaaagagacc 900
54 aaagtggagc tccgggagat gattgttcat gaacaagaaa gtgtgctaaa caaattagga 960
56 aagaacgact cttcatctga agaagaacag agagaagaaa aagccattgc taggccccgt 1020
58 cagcatttct ccagaagcaa gagaagcata ggagcaaacc actgtcggag aacgtcactc 1080
60 catgtgaact ttaaagaaat aggttgggat tcttggatca ttgcacccaa agattatgag 1140
62 gcttttgagt gtaaaggagg ttgtctcttc cccctcacag ataattgttac gccaaccaaa 1200
64 catgctattg tccagactct ggtgcatctc caaaacccaa agaaagcttc caaggcctgt 1260
66 tgtgttccaa ctaaattgga tgcaatctct attctttata aggatgatgc tgggtgtgcc 1320
68 actttgatat ataactatga agggatgaaa gtggcagaat gtggctgcag gtagtatatg 1380
70 ctgaatatct aagaatatat tcttttctgc tgtctgtgaa actgtacatt agtgatgcaa 1440
72 atgaaaaatc ttgcaaacaa ggtttggagc acggcatggg gctggttgtt gttgctgctt 1500
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79 <210> SEQ ID NO: 2
80 <211> LENGTH: 427

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81 <212> TYPE: PRT
82 <213> ORGANISM: Chick
84 <400> SEQUENCE: 2
86 Met His Tyr Phe Gly Val Leu Ala Ala Leu Ser Val Phe Asn Ile Ile
87 1 5 10 15
90 Ala Cys Leu Thr Arg Gly Lys Pro Leu Glu Asn Trp Lys Lys Leu Pro
91 20 25 30
94 Val Met Glu Glu Ser Asp Ala Phe Phe His Asp Pro Gly Glu Val Glu
95 35 40 45
98 His Asp Thr His Phe Asp Phe Lys Ser Phe Leu Glu Asn Met Lys Thr
99 50 55 60
102 Asp Leu Leu Arg Ser Leu Asn Leu Ser Arg Val Pro Ser Gln Val Lys
103 65 70 75 80
106 Thr Lys Glu Glu Pro Pro Gln Phe Met Ile Asp Leu Tyr Asn Arg Tyr
107 85 90 95
110 Thr Ala Asp Lys Ser Ser Ile Pro Ala Ser Asn Ile Val Arg Ser Phe
111 100 105 110
114 Ser Thr Glu Asp Val Val Ser Leu Ile Ser Pro Glu Glu His Ser Phe
115 115 120 125
118 Gln Lys His Ile Leu Leu Phe Asn Ile Ser Ile Pro Arg Tyr Glu Glu
119 130 135 140
122 Val Thr Arg Ala Glu Leu Arg Ile Phe Ile Ser Cys His Lys Glu Val
123 145 150 155 160
126 Gly Ser Pro Ser Arg Leu Glu Gly Asn Met Val Ile Tyr Asp Val Leu
127 165 170 175
130 Asp Gly Asp His Trp Glu Asn Lys Glu Ser Thr Lys Ser Leu Leu Val
131 180 185 190
134 Ser His Ser Ile Gln Asp Cys Gly Trp Glu Met Phe Glu Val Ser Ser
135 195 200 205
138 Ala Val Lys Arg Trp Val Lys Ala Asp Lys Met Lys Thr Lys Asn Lys
139 210 215 220
142 Leu Glu Val Val Ile Glu Ser Lys Asp Leu Ser Gly Phe Pro Cys Gly
143 225 230 235 240
146 Lys Leu Asp Ile Thr Val Thr His Asp Thr Lys Asn Leu Pro Leu Leu
147 245 250 255
150 Ile Val Phe Ser Asn Asp Arg Ser Asn Gly Thr Lys Glu Thr Lys Val
151 260 265 270
154 Glu Leu Arg Glu Met Ile Val His Glu Gln Glu Ser Val Leu Asn Lys
155 275 280 285
158 Leu Gly Lys Asn Asp Ser Ser Ser Glu Glu Glu Gln Arg Glu Glu Lys
159 290 295 300
162 Ala Ile Ala Arg Pro Arg Gln His Ser Ser Arg Ser Lys Arg Ser Ile
163 305 310 315 320
166 Gly Ala Asn His Cys Arg Arg Thr Ser Leu His Val Asn Phe Lys Glu
167 325 330 335
170 Ile Gly Trp Asp Ser Trp Ile Ile Ala Pro Lys Asp Tyr Glu Ala Phe
171 340 345 350
174 Glu Cys Lys Gly Gly Cys Phe Phe Pro Leu Thr Asp Asn Val Thr Pro
175 355 360 365

```

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```

178 Thr Lys His Ala Ile Val Gln Thr Leu Val His Leu Gln Asn Pro Lys
179      370                      375                      380
182 Lys Ala Ser Lys Ala Cys Cys Val Pro Thr Lys Leu Asp Ala Ile Ser
183 385                      390                      395                      400
186 Ile Leu Tyr Lys Asp Asp Ala Gly Val Pro Thr Leu Ile Tyr Asn Tyr
187                      405                      410                      415
190 Glu Gly Met Lys Val Ala Glu Cys Gly Cys Arg
191      420                      425

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194 <210> SEQ ID NO: 3

195 <211> LENGTH: 143

196 <212> TYPE: PRT

197 <213> ORGANISM: Artificial Sequence

199 <220> FEATURE:

200 <223> OTHER INFORMATION: COOH-terminus of BMP-2

202 <220> FEATURE:

203 <221> NAME/KEY: DOMAIN

204 <222> LOCATION: (1)..(143)

205 <223> OTHER INFORMATION:

208 <400> SEQUENCE: 3

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210 Glu His Ser Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His
211 1      5                      10                      15
214 Asp Gly Lys Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys
215      20                      25                      30
218 His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu
219      35                      40                      45
222 Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro
223      50                      55                      60
226 Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu
227 65                      70                      75                      80
230 Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val
231      85                      90                      95
234 Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu
235      100                     105                     110
238 Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val
239      115                     120                     125
242 Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
243      130                     135                     140

```

246 <210> SEQ ID NO: 4

247 <211> LENGTH: 143

248 <212> TYPE: PRT

249 <213> ORGANISM: Artificial Sequence

251 <220> FEATURE:

252 <223> OTHER INFORMATION: COOH-terminus of DPP

254 <220> FEATURE:

255 <221> NAME/KEY: DOMAIN

256 <222> LOCATION: (1)..(143)

257 <223> OTHER INFORMATION:

260 <400> SEQUENCE: 4

262 Asp Asp Gly Arg His Lys Ala Arg Ser Ile Arg Asp Val Ser Gly Gly

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Input Set : A:\40314-a.txt

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```

263 1          5          10          15
266 Glu Gly Gly Gly Lys Gly Gly Arg Asn Lys Arg His Ala Arg Arg Pro
267          20          25          30
270 Thr Arg Arg Lys Asn His Asp Asp Thr Cys Arg Arg His Ser Leu Tyr
271          35          40          45
274 Val Asp Phe Ser Asp Val Gly Trp Asp Asp Trp Ile Val Ala Pro Leu
275          50          55          60
278 Gly Tyr Asp Ala Tyr Tyr Cys His Gly Lys Cys Pro Phe Pro Leu Ala
279 65          70          75          80
282 Asp His Phe Asn Ser Thr Asn His Ala Val Val Gln Thr Leu Val Asn
283          85          90          95
286 Asn Met Asn Pro Gly Lys Val Pro Lys Ala Cys Cys Val Pro Thr Gln
287          100         105         110
290 Leu Asp Ser Val Ala Met Leu Tyr Leu Asn Asp Gln Ser Thr Val Val
291          115         120         125
294 Leu Lys Asn Tyr Gln Glu Met Thr Val Val Gly Cys Gly Cys Arg
295          130         135         140

```

298 <210> SEQ ID NO: 5

299 <211> LENGTH: 143

300 <212> TYPE: PRT

301 <213> ORGANISM: Artificial Sequence

303 <220> FEATURE:

304 <223> OTHER INFORMATION: COOH-terminus of BMP-6

306 <220> FEATURE:

307 <221> NAME/KEY: DOMAIN

308 <222> LOCATION: (1)..(143)

309 <223> OTHER INFORMATION:

312 <400> SEQUENCE: 5

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314 Arg Thr Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser Arg Asn
315 1          5          10          15
318 Arg Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp
319          20          25          30
322 Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu Leu Tyr
323          35          40          45
326 Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Lys
327          50          55          60
330 Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu Asn
331 65          70          75          80
334 Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
335          85          90          95
338 Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro Thr Lys
339          100         105         110
342 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile
343          115         120         125
346 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
347          130         135         140

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350 <210> SEQ ID NO: 6

351 <211> LENGTH: 144

352 <212> TYPE: PRT

RAW SEQUENCE LISTING

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Input Set : A:\40314-a.txt

Output Set: N:\CRF3\04082002\J002278.raw

353 <213> ORGANISM: Artificial Sequence

355 <220> FEATURE:

356 <223> OTHER INFORMATION: COOH-terminus of VG-1

358 <220> FEATURE:

359 <221> NAME/KEY: DOMAIN

360 <222> LOCATION: (1)..(143)

361 <223> OTHER INFORMATION:

364 <400> SEQUENCE: 6

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366 Glu Cys Lys Asp Ile Gln Thr Phe Leu Tyr Thr Ser Leu Leu Thr Val
367 1          5          10          15
370 Thr Leu Asn Pro Leu Arg Cys Lys Arg Pro Arg Arg Lys Arg Ser Tyr
371          20          25          30
374 Ser Lys Leu Pro Phe Thr Ala Ser Asn Ile Cys Lys Lys Arg His Leu
375          35          40          45
378 Tyr Val Glu Phe Lys Asp Val Gly Trp Gln Asn Trp Val Ile Ala Pro
379          50          55          60
382 Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly Glu Cys Pro Tyr Pro Leu
383 65          70          75          80
386 Thr Glu Ile Leu Asn Gly Ser Asn His Ala Ile Leu Gln Thr Leu Val
387          85          90          95
390 His Ser Ile Glu Pro Glu Asp Ile Pro Leu Pro Cys Cys Val Pro Thr
391          100         105         110
394 Lys Met Ser Pro Ile Ser Met Leu Phe Tyr Asp Asn Asn Asp Asn Val
395          115         120         125
398 Val Leu Arg His Tyr Glu Asn Met Ala Val Asp Glu Cys Gly Cys Arg
399          130         135         140

```

402 <210> SEQ ID NO: 7

403 <211> LENGTH: 147

404 <212> TYPE: PRT

405 <213> ORGANISM: Artificial Sequence

407 <220> FEATURE:

408 <223> OTHER INFORMATION: COOH-terminus of Activin-A

410 <220> FEATURE:

411 <221> NAME/KEY: DOMAIN

412 <222> LOCATION: (1)..(147)

413 <223> OTHER INFORMATION:

416 <400> SEQUENCE: 7

```

418 Gly Ala Asp Glu Glu Lys Glu Gln Ser His Arg Pro Phe Leu Met Leu
419 1          5          10          15
422 Gln Ala Arg Gln Ser Glu Asp His Pro His Arg Arg Arg Arg Arg Gly
423          20          25          30
426 Leu Glu Cys Asp Gly Lys Val Asn Ile Cys Cys Lys Lys Gln Phe Phe
427          35          40          45
430 Val Ser Phe Lys Asp Ile Gly Trp Asn Asp Trp Ile Ile Ala Pro Ser
431          50          55          60
434 Gly Tyr His Ala Asn Tyr Cys Glu Gly Glu Cys Pro Ser His Ile Ala
435 65          70          75          80
438 Gly Thr Ser Gly Ser Ser Leu Ser Phe His Ser Thr Val Ile Asn His
439          85          90          95

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/002,278

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